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The complex genetic landscapes of familial MDS and AML reveal pathogenic germline variants

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ABSTRACT

The inclusion of familial myeloid malignancies as a separate disease entity in the revised WHO classification has renewed efforts to improve the recognition and management of this group of at risk individuals. Here we report a cohort of 86 acute myeloid leukemia (AML) and myelodysplastic syndrome (MDS) families with 49 harboring germline variants in 16 previously defined loci (57%). Whole exome sequencing in a further 37 ‘uncharacterized’ families (43%) allowed us to rationalize 65 new candidate loci, including genes mutated in rare hematological syndromes (*ADA*, *GP6*, *IL17RA*, *PRF1* and *SEC23B*), reported in prior MDS/AML or inherited bone marrow failure series (*DNAH9*, *SH2B3* and *NAPRT1*) or variants at novel loci (*DHX34*) that appear specific to inherited forms of myeloid malignancies. Altogether, our series of MDS/AML families offer novel insights into the etiology of myeloid malignancies and provide a framework to prioritize variants for inclusion into routine diagnostics and patient management.

INTRODUCTION

Inherited forms of myeloid malignancies are thought to be rare, although the precise incidence and prevalence are not known. The inclusion of familial myeloid malignancies as a separate disease entity in the World Health Organization (WHO) classification of hematological cancers in 2016¹ and their recognition by the European Leukaemia Net (ELN)² has led to greater awareness of the existence of these heritable forms of disease. It also highlights the importance of early diagnosis and tailored management of this group of patients and families³. Not only can families benefit from appropriate genetic counseling and long-term surveillance, there are several examples reported in the literature of donor-derived malignancy following transplant⁴⁻⁶ from an asymptomatic family member and the benefit of modifying conditioning regimen in patients with an underlying telomerase mutation prior to bone marrow transplant⁷.

The clinical recognition of familial transmission is challenging as family sizes tend to be small with incidence frequently masked by marked differences in disease latency and phenotype exacerbated by the absence of routine customized familial diagnostic testing. The problem is more acute in the adult population compared with pediatric onset of disease, where there can be a heightened suspicion on behalf of the treating physician and where a malignancy can arise as part of a wider syndrome³. Many patients/families initially exhibiting bone marrow failure syndromes such as Fanconi anemia, dyskeratosis congenita, and Shwachman–Diamond syndrome are prone to the development of myelodysplastic syndrome (MDS) or acute myeloid leukemia (AML)⁸.

It is 20 years since inherited variants in the transcription factor *RUNX1* were identified as being responsible for familial platelet disorder with a propensity to develop AML (FPD-AML)⁹. Reflecting the uptake of next-generation sequencing approaches, we are now aware of more than 20 genes linked with

heritable myeloid malignancies⁸ (Table 1), with a significant number of newly described loci appearing restricted to a few core families (*ATG2B/GSK1P*¹⁰, *ETV6*^{11,12}, *SRP72*¹³). Several of these familial loci are also mutated in sporadic AML/MDS (*RUNX1*⁹, *CEBPA*¹⁴, *GATA2*¹⁵) while others appear enriched or exclusive to inherited forms of myeloid malignancies (*DDX41*¹⁶). These examples offer a unique insight into the underlying etiology of myeloid malignancies and present opportunities to understand disease latency, penetrance and the reasons behind the striking intra- and inter- clinical heterogeneity that is a feature of many of these families.

To address this issue, we have analyzed the largest series of AML/MDS families assembled to date. It exemplifies the molecular heterogeneity of inherited AML and MDS¹⁷, with likely pathogenic variants in 16 previously defined loci, detected in 49 (57%) families. Whole exome sequencing (WES) in a further 37 'uncharacterized' families (43%) focus attention to 144 variants in 65 candidate genes, 26 (40%) of which are mutated in cases of sporadic AML. This includes genes mutated in rare hematological syndromes (*ADA*, *GP6*, *IL17RA*, *PRF1* and *SEC23B*), reported in prior MDS/AML or inherited bone marrow failure (IBMF) series (*DNAH9*, *SH2B3* and *NAPRT1*) or novel loci where loss of function of the identified germline variants was demonstrated (*DHX34*).

RESULTS

Cohort of familial AML/MDS cases

In this study, "familial AML/MDS" references families where two or more family members (usually first-degree relatives) were diagnosed with a hematological disorder (predominantly AML, MDS, aplastic anemia or thrombocytopenia) with at least one of the affected cases being categorized as MDS or AML. Bone marrow, peripheral blood or other non-hematopoietic samples were collected from at least one affected individual from 86 families (FML001-086) and the corresponding laboratory and clinical information was collated to capture relevant information relating to patients and their relatives (Table 2; Supplementary Figs. 1, 2). Our cohort of cases has not been accrued as part of any systematic initiative, but instead, has been based on *ad hoc* referral of cases, that has spanned several years, from both UK and international institutions. Across our series of 86 families, we have collated 297 samples corresponding to 221 individuals, of which 168 were affected and 53 were unaffected (Supplementary Data 1). In 33 families, material was available on the index case only. In 5 additional cases, we have samples on the index case and at least one additional unaffected individual. In the remaining 48 families, our collection includes samples from multiple affected individuals allowing us to perform segregation analysis on identified variants. For simplicity, we have assigned our families into two discrete groups (Table 1) based on the panel used for clinical indication 'R347 Inherited predisposition to acute myeloid leukaemia (AML)' in the NHS England Genomic Medicine Service [<https://www.england.nhs.uk/publication/national->

[genomic-test-directories/](#). Group 1, where a variant has been detected either at a locus with high/moderate level of evidence for gene-disease association, or that is emerging from basic research or mutated in other inherited hematological syndromes (FML001-FML049; Fig. 1; Supplementary Fig. 1; Supplementary Data 2); and Group 2, where the molecular lesion has not been defined (FML050-FML086; Supplementary Fig. 2; Supplementary Data 3).

Group 1 families with variants in established genes

Of the 49 Group 1 families (Fig. 1; Supplementary Fig. 1; Supplementary Data 2), 32 have been reported previously as part of previous published studies^{9,13,14,18-32}. The additional 17 families (Fig. 2; Table 3; Supplementary Data 4) harbor variants in 13 discrete loci and together highlight the high index of suspicion needed on behalf of the treating physician, to infer an inherited malignancy and warrant further investigation. The clinical heterogeneity is reflected in variations in age of onset from 1-68 years, MDS/AML co-occurring with other non-hematological features in 6 families (FML019, FML037, FML041, FML044, FML045 and FML047) and variable penetrance observed in 4 families (FML007, FML014, FML018 and FML041) (Fig. 2; Table 3; Supplementary Data 2).

Family FML007 represents the second example of a C-terminal *CEBPA* germline variant, p.Gln330Argfs*74, that is associated with reduced penetrance (over 50% of carriers are asymptomatic) AML (Fig. 2a). This is in contrast to the more conventional near fully penetrant N-terminal variants³³, seen in most examples of pure familial *CEBPA* AML. *DDX41* variants were detected in probands from FML012 (p.Met1?) and FML013 (p.Arg124*) (Fig. 2b and 2c), with both affected patients diagnosed with MDS at 68 years. The heritable presentation in this family could be easily overlooked in favor of sporadic disease due to its unusual late onset¹⁷. The heterozygous germline *GATA2* variant p.Thr354Met, present in both the index case (III.1) and his asymptomatic father (II.2) of family FML018 (Fig. 2e), represents a further example of reduced penetrance linked to this particular missense *GATA2* variant where variable penetrance has been associated with fluctuations in the expression of the mutated allele³⁴. The occurrence of MDS/AML in certain families may also coincide with other non-hematological features: the index case of family FML019 presented with MDS and congenital deafness, analogous to a case reported by Saida *et al.*³⁵ in a family with the identical germline *GATA2* variant (p.Arg362*) (Fig. 2f). In family FML037, harboring a novel *TERC* variant n.179_180delinsGG (absent in ExAC database) (Fig. 2l), both affected individuals (II.2 and II.1) were prematurely gray in their 20's, a feature frequently associated with *TERC* and *TERT* variants. Our series also includes three examples of FPD-AML (FML029, FML030 and FML031) where sequencing analysis failed to detect any *RUNX1* variants (Fig. 2g-i; Supplementary Data 2).

Familial platelet disorder with predisposition to myeloid malignancy (FPDMM) is normally associated with germline *RUNX1* variants and characterized by life-long moderate thrombocytopenia and platelet function defects with heterogeneity both in age and presentation and significant risk of MDS/AML transformation, estimated at 20-60%⁸. Although most of the FPDMM families harbor germline *RUNX1* variants, inherited large intragenic duplications or deletions have been also described in these families³⁶⁻³⁹. Therefore, we performed a subsequent profiling to detect large copy number variants and we identified novel germline *RUNX1* deletions in the three families with FPD-AML. A *RUNX1* deletion (chr21:36349450-36572837) was detected in patient II.5 of family FML029 (Fig. 2h; Supplementary Fig. 3a) and confirmed in other affected family members (III.2, III.3 and III.4) (Supplementary Fig. 3b). In family FML030, a *RUNX1* deletion was observed in II.2 that was absent in his healthy sister (II.1) (Fig. 2g; Supplementary Fig. 3). Peripheral blood and salivary DNA from II.2 of family FML031 revealed a *RUNX1* 666kb deletion (chr21: 36389457- 37055677) (Fig. 2i; Supplementary Fig. 3). Altogether, a comparison of breakpoints in the three families revealed a ‘hotspot’ for constitutional deletion, with a common deleted segment spanning ~100kb (chr21: 36400658-36572837) that encompasses the distal *RUNX1* promoter and first two exons. These results highlight the importance of performing copy number assessment in families or individuals who present with an appropriate clinical phenotype.

Identifying new candidate genes in Group 2 families

We performed whole exome sequencing (WES) analysis in the remaining 37 families (FML050-FML086; EGAD00001004539; Supplementary Fig. 2; Supplementary Data 3) where we had failed to detect a mutation in any of the Group 1 genes. It’s worth noting that we cannot rule out the possibility that our discovery series includes cases of known loci where CNVs or non-coding gene regulatory mutations represent novel molecular mechanisms which would go undetected using a coding-only screening strategy, or indeed the co-occurrence of independent sporadic cases of disease in the same family. In Group 2, we did not include families where we had assigned a variant to a category of ‘variant of unknown significance’ (VUS). In FML014 for example (Fig. 2d), the index case (IV.2) retained a novel heterozygous germline *ETV6* variant c.349C>T (p.Leu117Phe) with low ExAC frequency (8.237E-06) but samples from other affected family members (maternal grandfather (II.2), maternal great aunt (II.3) and maternal great-grandmother (I.2)) who had all died of leukemia, were unavailable. This exemplifies the inherent problems in classifying variants as well as searching for new loci in families where the molecular lesion has not been described or when material is limited and there is too great a reliance on the index case.

Our WES data suggests that there is no single gene that can account for the large number of unattributed heritable cases in our series. We observed on average 311 rare single nucleotide variants (minor allele frequency <0.005, range 161-781) per patient. In order to identify variants with a causative role in familial MDS/AML, we applied the following criteria (Supplementary Fig. 4): (i) demonstrated variant allele frequencies >30%, (ii) indels (6.2%), nonsense (2.4%) or splicing (+/- 1, 2 or 3) (5.1%) variants affecting the canonical transcript, (iii) segregated with the disease where testing was possible, (iv) a frequency of <0.0001 in population controls (ExAC database), (v) predicted to be pathogenic with two out of four tools used for functional annotation (PolyPhen2, MutationTaster, SIFT and Provean) and (vi) detected in the same gene in at least two families. In order to mitigate the large number of missense variants (86.3%), genes were only included if missense variants were detected in three or more families. These criteria defined 130 variants in 52 candidate genes (Supplementary Data 5). We also took advantage of other published series, cross referencing our WES data with the familial MDS/AML candidate loci selected by Churpek *et al.*⁴⁰, the potential candidate gene in the MDS/AML family described by Patnaik *et al.*⁴¹ and the causal, likely causal or possibly contributing genes identified in a cohort of inherited BMF patients by Bluteau *et al.*⁴² (Supplementary Data 6). This has allowed us to include an additional 13 genes, overlapping with these previous studies (Supplementary Data 7).

The combination of both criteria resulted in a final list of 144 variants in 65 genes across 34 of the 37 families (Supplementary Fig. 5; Supplementary Data 8). Multiple variants were detected in the majority of families (30/37) with no variant observed in FML052, 060 and 066. All variants selected for Sanger sequencing were validated (n=48) and segregation analysis confirmed the germline transmission in all cases tested where material was available from more than one affected individual (Supplementary Fig. 6). Consistent with the germline origin, the median VAF of all 144 variants was 0.48. Twenty six (40%) of the 65 genes were previously reported to be mutated in at least one example of sporadic AML from TCGA⁴³ and Tyner *et al.*⁴⁴ data (frequency ranged from 0.1 to 11%) (Supplementary Fig. 5; Supplementary Data 8). Following the recent study describing a synonymous *GATA2* germline variant affecting RNA splicing in a MDS/AML family⁴⁵, for completeness, we also performed an *in silico* analysis of our WES results using the Annovar tool⁴⁶ and the RefSeq Database⁴⁷ identifying 39 novel splicing synonymous variants (Supplementary Data 9), none of which arose in either *GATA2* or any other Group 1 loci.

Rationalizing candidate genes into discrete groups

We next sought to rationalize these 65 candidate genes by dividing them into 2 discrete groups based on an association with rare hematological syndromes (i) and a relevant function and/or mutated in three or

more families (ii) (Supplementary Fig. 4). Firstly, germline variants in 26 of the selected 65 genes (40%) have been implicated across a broad range of inherited disorders (Supplementary Data 8). Notably, five genes with germline variants in 10 families, *ADA*, *GP6*, *IL17RA*, *PRF1* and *SEC23B*, have been linked with autosomal recessive hematological syndromes (Fig. 3): T cell-negative, B cell-negative, natural killer cell-negative severe combined immunodeficiency (*ADA*, with novel heterozygous loss of function variants in our families FML056 (p.Gln3*) and FML071 (p.Glu88Argfs*34)); Platelet-type bleeding disorder-11 (*GP6*, mutated in families FML055 (p.Arg159*) and FML063 (p.Met430Lys)); Immunodeficiency-51 (IMD51) (*IL17RA*, with variants in families FML050, FML053 and FML068)), Familial hemophagocytic lymphohistiocytosis-2 (FHL2) (*PRF1*, mutated in family FML085 (p.Glu275Lys) and one family presented by Bluteau *et al.*⁴² (p.Asn252Ser); and Congenital Dyserythropoietic Anemia Type II (*SEC23B*, with variants in families FML061 (p.Pro542Leu) and FML062 (p.Glu361Asp)) (Fig. 3; Supplementary Data 8).

Among the non-syndromic genes, we noted *DNAH9* with variants in 3 families, a gene that interacts with the hematopoietic regulator BCL6⁴⁸ and is also mutated in one of the families described by Churpek *et al.*⁴⁰. In another family we identified a variant in *SH2B3* (p.Ala49Thr), implicated in hematopoietic stem cell self-renewal and quiescence through direct interaction with JAK2⁴⁹⁻⁵¹, with the variant adjacent to a frameshift variant described by Bluteau *et al.*⁴² (p.Arg50Glyfs*147) (Fig. 3). We also noted a germline duplication in *NAPRT1*, a major enzyme in cellular metabolism⁵², in one additional family (FML064, p.Val216_Phe219dup), highlighting its candidacy as it was previously found to be mutated (p.Arg405*) in the affected members of an MDS/AML family described by Patnaik *et al.*⁴¹ (Fig. 3; Supplementary Data 8). We also identified three families with variants in *TET2*, an epigenetic modifier that is recurrently mutated in sporadic AML and clonal hematopoiesis of indeterminate potential (CHIP), but whose germline variants may constitute a predisposing factor for myeloid neoplasm⁵³. Segregation of *TET2* variant in FML054 was demonstrated by Sanger sequencing in individuals I.1 and II.2 (Supplementary Fig. 6), but, we could not discount a CHIP origin of the *TET2* variants in families FML075 and FML081 (VAFs of 0.46 and 0.49, respectively).

Variants in the Nonsense-mediated RNA decay regulator *DHX34*

Four families harbored heterozygous variants in *DHX34* (p.Tyr515Cys, p.Arg897Cys, p.Asp638Asn and p.Glu444Asp), an RNA helicase that was shown to have a functional role in the nonsense-mediated RNA decay pathway (NMD)^{54,55} (Fig. 4a; Supplementary Data 8). The clinical features of the families were overlapping, with early disease onset. The index case in FML071 (II.2; Supplementary Data 3; Supplementary Fig. 2) was initially found to have thrombocytopenia, which progressed to pancytopenia

with hypocellular BM and tri-lineage myelodysplasia at age 10 years. Cytogenetic analysis showed monosomy 7 in ~10% of BM cells. She died of pulmonary complications post-SCT. Her older brother (II.1) had a similar hematological profile, presenting first with thrombocytopenia and at age 5 years had a hypocellular BM, dysplasia and monosomy 7. He died aged 11 years. In family FML061 (Supplementary Data 3; Supplementary Fig. 2), the index case (II.1) aged 2 years had intermittent neutropenia, anemia with macrocytosis and thrombocytopenia. The BM cellularity was reduced with tri-lineage dysplasia and monosomy 7. Her mother (I.1) was diagnosed with AML (sub-type M5) aged 10 years. She was treated successfully with chemotherapy. The index case in FML065 (II.1; Supplementary Data 3; Supplementary Fig. 2) aged 7 years had pancytopenia and was diagnosed to have AML with normal karyotype. His father (I.2) had been diagnosed to have hypocellular myelodysplasia. In the fourth family (FML055), the index case (II.2) was found to have pancytopenia aged 22 years. Bone marrow examination showed he had acute mixed lineage leukemia which was refractory to chemotherapy. His older brother (II.1) was diagnosed with AML aged 23 years. He died from complications post-SCT. Patients with heterozygous *DHX34* variants had no extra-hematopoietic abnormalities and no acquired variants in any of the 33 genes frequently mutated in MDS/AML analysed by targeted sequencing, apart from an *ASXL1* frameshift insertion (p.Gly646Trpfs*12) (VAF 12.7% and ExAC frequency of 0.0016) identified in the index case (II.1) of family FML061. It is noteworthy, the index cases of two families (FML061 and FML071) had monosomy 7 and cytogenetic data was unavailable for the other two families.

Previously, we have shown that *DHX34* is a *bona fide* NMD factor that acts in concert with core NMD factors to regulate a significant number of endogenous RNA targets in *C. elegans*, zebrafish and human cells^{56,57}. *DHX34*, a member of the DExH/D box family of RNA helicases, promotes remodeling of messenger ribonucleoproteins (mRNPs) during NMD. At the molecular level, *DHX34* induces a series of molecular transitions that result in an increased phosphorylation of the core NMD factor, UPF1, and leads to an enhanced recruitment of the NMD factors UPF2 and UPF3 to UPF1^{55,58}. These events are required for targeting aberrant mRNAs for degradation. All four *DHX34* variants identified in our families, compromised NMD activity, as shown by their failure to promote phosphorylation of UPF1 to levels induced by the wild-type protein (Fig. 4b and c), despite retaining the ability to bind UPF1 (Fig. 4d). Importantly, we also show that all four *DHX34* variants display a reduced recruitment of UPF2 and UPF3B to UPF1 (Supplementary Fig. 7).

DISCUSSION

While the coding landscape of somatic cases of myeloid malignancies is complete, we are still some way behind in cataloguing the germline and somatic variants that arise in familial presentations of these diseases. The inclusion by the WHO of inherited forms of MDS/AML as an independent entity

represented an important step forward and created a heightened awareness of this group of at risk individuals¹, so that today, with the application of NGS, more than 20 different loci of varying frequency have been linked to the occurrence of these familial diseases (Group 1; Table 1). There is a growing suspicion that the familial occurrence of AML/MDS is underappreciated clinically³; however, in the absence of large collections of well annotated cases and comprehensive gene discovery programs, it will be challenging to define with confidence the precise contribution of this group of patients to MDS/AML and to optimally manage patients and at risk family members. In our study, we have started to address this gap in knowledge by profiling the coding genome in 86 families with a history of myeloid disease. We report several new predisposing candidate genes in familial MDS/AML and note a significant overlap between the genetics of MDS/AML, inherited BMF syndromes and certain rare hematological syndromes (Fig. 3). These studies also pinpoint new biological mechanisms that appear to be specific to inherited forms of myeloid malignancies, including variants in the RNA helicase, *DHX34*, detected in 4 families, which impact the activity of the NMD pathway.

Overall, the pace of progress in the field of familial AML/MDS is hindered by the need for robust collection of samples, both from affected and unaffected family members and of diseased and healthy tissue, in order to discriminate germline from somatic changes, and passengers from pathogenic variants. Access to large multigenerational families is typically rare and while we have collected material on multiple affected individuals in many families, a reliance on material from a single index case remains problematic. While the availability of fibroblasts offers a gold standard approach to discriminate germline from somatic changes¹⁷, this was not practical in our series, reflecting for the most part the historical nature of our collections. We relied on confirming the germline origin of variants by segregation analysis where material was available from multiple affected individuals. In some cases, samples were available from a single affected and unaffected family member, and while these may be informative, caution is also required since reduced penetrance or late onset of overt disease is a feature of existing Group 1 loci that includes the *GATA2*³⁴, *DDX41*⁵⁹ and C-terminal *CEBPA*³³ mutations.

The candidate variants arising in our 37 discovery families exhibit a broad range of biological functions and, in some instances, have been implicated in malignant and non-malignant hematological disease (Supplementary Data 8). The confident prediction of new candidate genes is hindered by the presence of multiple variants in individual families (3.9 variants per family on average, range 1-16) and that many of the corresponding genes may not have an obvious functional association with hematopoiesis. Some candidate genes have been linked with hematological syndromes including *GP6* (FML055 and FML063), a glycoprotein receptor involved in platelet-collagen interactions during thrombus formation, mutated in platelet-type bleeding disorder-11⁶⁰; *SEC23B* (FML061 and FML062), a component of the transport vesicle coat protein complex II (COPII), mutated in dyserythropoietic anemia type II (CDAIL)⁶¹; *ADA* (FML056 and

FML071), a causative factor of T cell-negative, B cell-negative, natural killer cell-negative severe combined immunodeficiency⁶²; *IL17RA* whose homozygous germline variants are the cause of Immunodeficiency-51 (IMD51); and *PRF1* (FML085) associated with familial hemophagocytic lymphohistiocytosis-2 (FHL2). Such variants highlight the phenotypic complexity that can accompany specific gene variants and it's noteworthy that in all of these cases the referring center did not observe any features of immunodeficiency or other gene-specific features. Overall, it was highly informative to cross-reference our series of variants with other discovery cohorts of familial MDS/AML or IBMF syndromes. Bluteau and colleagues reported a variant in *SH2B3*⁴², which is a recognized negative regulator of normal hematopoiesis that is expressed in HSCs and progenitors. *SH2B3* is mutated in 5-7% of myeloproliferative disorders, lymphoid leukemia and the non-malignant disease idiopathic erythrocytosis⁶³. The variant in our study (FML085, p.Ala49Thr), which is adjacent to the one reported by Bluteau *et al.*⁴², locates to the dimerization domain of this adapter protein and appears distinct from the variants reported in myeloproliferative neoplasms that predominate in the PH and SH2 domains⁶³.

No variants met our selection criteria in three families, FML052, 060 and 066 and these examples highlight perfectly the challenges faced by researchers in identifying predisposing lesions. It's conceivable that such families may not represent *bona fide* familial disease and instead result from multiple sporadic examples of disease in the same family. It is also feasible that the variants may reside outside of the coding region, as seen with *GATA2*⁶⁴⁻⁶⁶, or reflect CNVs, as shown in examples of *RUNX1* mediated FPD³⁶. Equally we cannot rule out the possibility that a variant is private to a particular family; we would have overlooked the candidacy of *NAPRT1* in FML064 (p.Val216_Phe219dup) were it not for another variant (p.Arg405*) being recently reported in the same gene in an MDS/AML family by the group of Patnaik and colleagues.⁴¹ This gene encodes a NAD salvage enzyme and is reminiscent of some of the recent Group 1 loci, including *DDX41*¹⁶, as having no immediate functional association to AML/MDS. Such examples highlight the benefits of pooling data across series of patients and the importance of international collaborations, in order to focus attention on specific variants that co-occur across families, which may in the longer term gain acceptance as a Group 1 locus, while the validation of rare or private gene variation will always be challenging.

We functionally validated heterozygous variants in the RNA helicase *DHX34*, detected in four families, all of which impacted activity of the NMD (nonsense-mediated mRNA decay) pathway. NMD is a quality control mechanism that targets mRNAs that contain premature termination codons (PTCs) for degradation, but also regulates the expression levels of a large number of naturally occurring transcripts⁶⁷. Phosphorylation of the core NMD factor UPF1 is essential for NMD activation, since this event represses further translation initiation and triggers mRNA decay⁶⁸. Importantly, we show that all four DHX34 variants have a reduced effect on UPF1 phosphorylation (Fig. 4) and also display diminished

recruitment of UPF2, indicating a decreased NMD activity (Supplementary Fig. 7). Interestingly, variants in another RNA helicase, *DDX41*, is now a recognized loci in familial and acquired cases of MDS and AML¹⁶. *DHX34*, does however, belong to a different family of RNA helicases, the DExH/D type of proteins⁶⁹, and besides its reported role in NMD, has also been identified as a component of the spliceosomal complex C, suggesting its involvement in pre-mRNA splicing⁷⁰. The reported variants in *DDX41* also give rise to defects in pre-mRNA splicing and, given the prevalence of mutations in pre-mRNA splicing factors in MDS/AML patients⁷¹, one possibility is that splicing defects caused by mutations in *DHX34* may be one way by which these germline variants contribute to pathogenesis.

While this new knowledge may well prove important for the respective families where awareness may prevent the occurrence of donor-derived disease following selection of asymptomatic donors and improve the overall management of this patient group, it is important not to over emphasize the individual impact of variants reported in our study. In a broader scheme, resolving germline predisposition can offer new insights into the etiology of acute leukemia, seen recently with *DDX41*¹⁶ and *SAMD9L*^{72,73} variants, and shed light on the mechanisms that underpin disease latency, penetrance and intra-clinical heterogeneity, given that the disease arises from the same initiating gene mutation. We are some way off from defining the actual frequency of familial AML/MDS and in the future, large studies like the HARMONY Alliance programme (<https://www.harmony-alliance.eu/>), a European Network of Excellence that is collecting information on 7 hematological malignancies including MDS and AML, may provide the resources necessary to rationalize patients into distinct familial and sporadic groups and address the question of the incidence of these forms of AML/MDS. Altogether, this new data represents an important step forward in developing tailored diagnosis for familial MDS/AML while providing insights into the etiology of myeloid malignancies and a framework on which to integrate and prioritize genetic variants emerging from research and predisposing to these diseases.

METHODS

Patients and families

221 individuals from 86 families were included in the study (Supplementary Data 1, 2; Supplementary Figs.1, 2). In each family, two or more family members (usually first-degree relatives) were diagnosed with a hematological disorder (predominantly AML, MDS, aplastic anemia or thrombocytopenia) with at least one of the affected cases being categorized as MDS or AML. Patients and asymptomatic members of the families included in the study gave written consent under the approval of our local research ethics committee (London – City and East, REC reference 07/Q0603/5). Exome sequencing and candidate gene sequencing was performed using genomic DNA obtained from whole peripheral blood or bone marrow aspirates.

Targeted sequencing

Targeted sequencing of 10 known disease genes (*ACD*, *ANKRD26*, *CEBPA*, *DDX41*, *ETV6*, *GATA2*, *RUNX1*, *SRP72*, *TERC* and *TERT*) was performed for the index case of each family using the accredited testing facility at the West Midlands Regional Genetics Laboratories (WMRGL) in Birmingham, UK [https://www.geneadviser.com/geneticstest/familial_mds_familial_aml_sequencing_birmingham].

Variants were considered pathogenic if they had been previously described to be associated with familial MDS/AML or new variants (SNVs or indels) meeting the following criteria: (1) minor allele frequency in healthy population (ExAC and gnomAD databases) <0.00001, (2) Variant Allele Frequency >30%, (3) Predicted to be pathogenic with two out of four tools for functional annotation (PolyPhen2, MutationTaster, SIFT and Provean), (4) sufficient evidence of pathogenicity and not meeting any criteria for a benign assertion following ACMG guidelines⁷⁴, and (5) where practical, the segregation with affected individuals.

A targeted myeloid panel of 33 genes frequently mutated in MDS/AML (*ASXL1* (exon 12), *BCOR* (all), *CALR* (exon 9), *CBL* (exons 7 + 8 + 9), *CEBPA* (all), *CSF3R* (exons 14 – 17), *DNMT3A* (all), *ETV6* (all), *EZH2* (all), *FLT3* (exons 14 + 15 + 20), *GATA2* (all), *GNAS* (exons 8 + 9), *IDH1* (exon 4), *IDH2* (exon 4), *IKZF1* (all), *JAK2* (exons 12 + 14), *KIT* (exons 2, 8-11, 13 + 17), *KRAS* (exons 2 + 3), *MPL* (exon 10), *NPM1* (exon 12), *NRAS* (exons 2 + 3), *PDGFRA* (exons 12, 14, 18), *PHF6* (all), *PTPN11* (exons 3 + 13), *RUNX1* (all), *SETBP1* (exon 4), *SF3B1* (exons 12 – 16), *SRSF2* (exon 1), *TET2* (all), *TP53* (all), *U2AF1* (exons 2 + 6), *WT1* (exons 7 + 9) and *ZRSR2* (all)) was employed to determine the acquired variants in the five patients with germline *DHX34* variants. An in-house True SeqCustom Amplicon (TSCA) design (Illumina, San Diego, California, USA) was used for target enrichment. Pooled library targets were sequenced the MiSeq sequencing platform. Minimum read depth threshold was 150 reads; lower limit of sensitivity was 5-10% variant allele frequency (VAF).

Whole Exome Sequencing

Whole exome sequencing (WES) libraries were prepared from 200 ng of genomic DNA using the Agilent SureSelect^{XT} Target Enrichment System for Illumina Paired-End Multiplexed Sequencing Library coupled with the Agilent SureSelect^{XT} Human all exon v6 capture reagent. Libraries were sequenced on a NextSeq 550 sequencer using the High output 300 cycles kit generating 150 bp paired end single-indexed reads.

WES data were processed according to the pipeline described in Pontikos *et al.*⁷⁵ available at [https://github.com/UCLGeneticsInstitute/DNASeq_pipeline]. In brief, short read data were aligned using Novoalign (version 3.02.08). Variants and indels were called according to GATK (version 3.5) best practice⁷⁶. Joint calling and variant quality score recalibration was performed with a set of 2,500 WES internal control samples from the UCLex consortium in order to minimize platform specific variants and artefactual batch effects. The variants were then annotated using the Variant Effect Predictor⁷⁷, output to

JSON format, post processed by a Python script and loaded into a Mongo database. The filtering was performed using a bespoke R script to filter out variants. An external allele frequency threshold of less than 0.005 or missing from ExAC and GnomAD was applied. Variants with a sequencing depth less than 20 or in segmental duplicated regions of the genome were also filtered out.

Sanger sequencing

48 selected variants identified by WES in 23 candidate genes were validated by Sanger sequencing (Supplementary Fig. 6). PCR reactions to amplify each variant were performed using 1.1x ReddyMix™ (Life Technologies) and purified PCR fragments (QIAquick Gel Extraction Kit, QIAGEN, Venlo, Netherlands) were sequenced by GATC Biotech (Eurofins, Ebersberg, Germany). Sequences of the oligonucleotides used are shown in Supplementary Data 10.

RUNX1 deletions detection: Array CGH, SNP-array and MLPA

As our targeted sequencing panel did not capture structural abnormalities, a combination of comparative genomic hybridization array (Array CGH) or SNP array and Multiplex Ligation-dependent Probe Amplification (MLPA) was used to identify germline *RUNX1* deletions in the three families with clinical characteristics of familial platelet disorder with predisposition to myeloid malignancy (FPDMM) from our cohort (FML029, FML030 and FML031). A customized 2x400k oligo-array, Agilent™ was used in families FML029 (II.5) and FML031 (II.2) to analyze genes where CNAs have been associated with familial MDS/AML and IBMF syndromes (*RUNX1*, *GATA2*, *CEBPA*, *SRP9*, *SRP14*, *SRP19*, *SRP54*, *SRP68*, *SRP72*, *MPL*, *DKC1*, *TERT*, *TERC*, *NOP10*, *NHP2*, *TINF2*, *CTC1*, *C16ORF57*, *TCAB1*). DNA sample from II.2 of family FML030 was hybridized to the The Affymetrix Cytoscan HD array according to the manufacturer's protocols. Copy number analysis was performed using Affymetrix chromosome analysis suite (CHAS) v 2.1. An MLPA assay customized for familial MDS/AML loci (P437-A1 Probemix, MRC Holland) was used for verification and segregation analysis (where possible) of the novel *RUNX1* deletions identified in the three families. Raw data obtained from each sample were analyzed using Peak Scanner software v1.0 (Applied Biosystems, CA). (Supplementary Fig. 3).

Telomere length measurement

Telomere length measurement was performed using a monochrome multiplex quantitative PCR method⁷⁸. Briefly, the amount of telomeric DNA (T) and the amount of a single copy gene (S) were quantified in each genomic DNA sample, using standard curves in a real-time PCR reaction (Roche

LightCycler). This gave a T/S ratio, which is proportional to the telomere length. Samples were run in quadruplicate and compared to the range of T/S ratios obtained from 225 healthy controls.

DHX34 functional validation

The plasmids pcG T7-DHX34, pcDNA3-3XFLAG-UPF1 constructs and siRNA have been described previously⁵⁵. The DHX34 variants were cloned by PCR amplification, using full-length *DHX34*, as a template. Primer sequences are available upon request. For UPF1 phosphorylation and UPF2 and UPF3 recruitment experiments, HEK293T cells grown in six well plates were first transfected with 25 nM of siRNA using Dharmafect I (Life Technologies) following manufacturer's instructions and expanded 24h later. After 72h cells were subsequently transfected with 75 nM siRNA, together with 20 µg of pcDNA3xFLAG-UPF1, and 20 µg of a plasmid expressing either siRNA-resistant wild-type or mutant T7-DHX34 protein, also including empty vector controls. Cells were harvested 48h later for FLAG-Immunoprecipitation using Anti-FLAG M2 Affinity Gel (A2220, Sigma-Aldrich). Protein complexes were analyzed by Western Blotting and UPF1 phosphorylation was detected using Phospho-(Ser/Thr) ATM/ATR Substrate (2851, Cell Signaling) antibodies. FLAG-UPF1 levels in the Immunoprecipitations were detected with anti-FLAG (F1804, M2 clone, Sigma-Aldrich), and further probed with anti-UPF2 (sc-20227, Santa Cruz) and anti-UPF3B (sc-48800, Santa Cruz) antibodies, as previously described⁵⁵. Signals were detected with the ImageQuant LAS 4000 system (GE Healthcare) and quantified using the ImageQuant TL Software (GE Healthcare). For FLAG-UPF1 and T7-DHX34 co-Immunoprecipitations, cells grown in 6-well plates were transfected with 1 µg pcneo-FLAG-UPF1 and 1 µg T7-DHX34 constructs or the corresponding empty vector plasmids. Cells were expanded 24h after and harvested 48h after transfection. FLAG-UPF1 and T7-DHX34 constructs were detected using anti-FLAG or anti-DHX34 antibodies (non-commercial antibody described previously by Hug and Caceres)⁵⁵. All antibodies were used at 1/1000 dilution.

DATA AVAILABILITY

The whole-exome sequencing data have been deposited in the EGA database under the accession code EGAS00001003399 [<https://ega-archive.org/studies/EGAS00001003399>]. Other datasets referenced during the study are available from TCGA⁴³ [<https://portal.gdc.cancer.gov/projects/TCGA-LAML>] and BeatAML from Tyner *et al.*⁴⁴ [<http://www.vizome.org/aml/>]. The remainder, supporting the findings of this study, are available within the article and its supplementary information files with information corresponding to individual samples accessible through the corresponding author, upon reasonable request. Images of uncropped western blots underlying Figs. 4b and 4d and Supplementary Fig.7 are provided as a Source Data File. A reporting summary for this article is available as a Supplementary Information file.

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AUTHOR CONTRIBUTIONS

ID, TV, JF conceived the project. JF, AR-M, ID and TV designed the project and wrote the manuscript. AR-M, KT, SC, AE, AW and HT performed research and collected data. A.F.A.S, JA and AH contributed to data collection. NH and JFC designed and performed the experiments for *DHX34* functional validation. JM, PP, SEA and KR performed targeted sequencing. NP, VP, JW, AR-M, TV and FC performed data analysis. MB, AB, CB, DB, PF, AG, AH, HH-H, UH, SK, SL, ML, AMM, JM, PM, RM, JFN, CO, JP, EP, CP, RP, NP-M, AR, NR, AS, GS, DT, CT, AU, PV, BS, TR, DS, JW and JDC contributed with patient samples.

COMPETING INTERESTS

The authors declare no competing interests.

FIGURE LEGENDS

Figure 1: Group 1 families: Families with variants in established genes. a, Number of families with variants in known disease-causing loci. In grey, genes where the level of evidence for gene-disease association is high; moderate level of evidence in blue; and genes emerging from basic research or mutated in other inherited hematological syndromes with high risk of MDS/AML, in red. Variants in these genes are heterozygous, apart from for *ERCC6L2*, *FANCA* and *SBDS* where they are biallelic, and for *WAS* where it is hemizygous. b, Percentages of our family cohort with causal variants in known disease-causing genes.

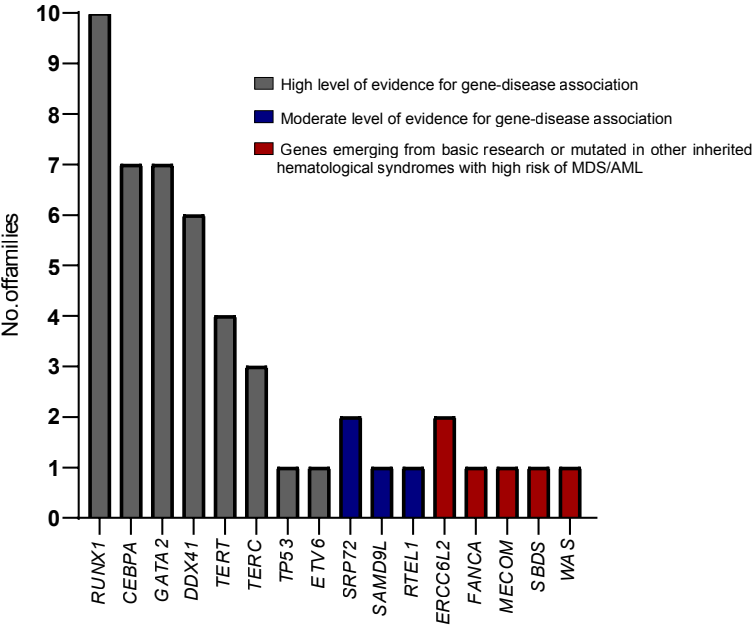
Figure 2: Unreported families with variants in established loci. Pedigree representation of the 17 newly described families that include one additional *CEBPA* family (c.1138_988dupGAAC:p.Gln330Argfs*74) (a), two *DDX41* (c.3G>A:p.Met1? and c.370C>T:p.Arg124X) (b, c), one *ETV6* (c.349C>T:p.Leu117Phe) (d), two *GATA2* (c.1061C>T:p.Thr354Met and c.1084C>T:p.Arg362X) (e, f), three *RUNX1* (*RUNX1* deletions: del(21):36349450-36572837, del(21):36400658-36972948 and del(21):36389492-37056053) (g, h, i), one *SAMD9L* (c.4418G>A:p.Ser1473Asn) (j), one *TERT* (c.1445delA:p.His482Profs*27) (k), one *TERC* (r.179_180TCdelinsGG) (l), one *MECOM* (c.2443C>T:p.Arg815Trp) (m), one *FANCA* (c.2505-1G>T/c.3626+5G>C) (n), one *SBDS* (c.258+2T>C/c.183_184delinsCT:p.Lys62X) (o), one *WAS* (c.1336delA:p.Lys446fs) (p), and one *TP53* (c.844C>T:p.Arg282Trp) (q). Age of the patients is indicated as a number in grey font color and italic. Index case of each family is indicated with an arrow.

Figure 3: Summary of disease-genes and new candidate genes mutated in our cohort of MDS/AML families. Schematic representation of established disease-genes (Group 1) and new candidate genes (Group 2) that are mutated in our cohort of MDS/AML families, and their overlap with classical inherited BMF syndromes based on Bluteau *et al.* classification⁴² (blue), or other inherited hematological disorders (pink). In orange font, genes reported to be frequently mutated in sporadic AML.

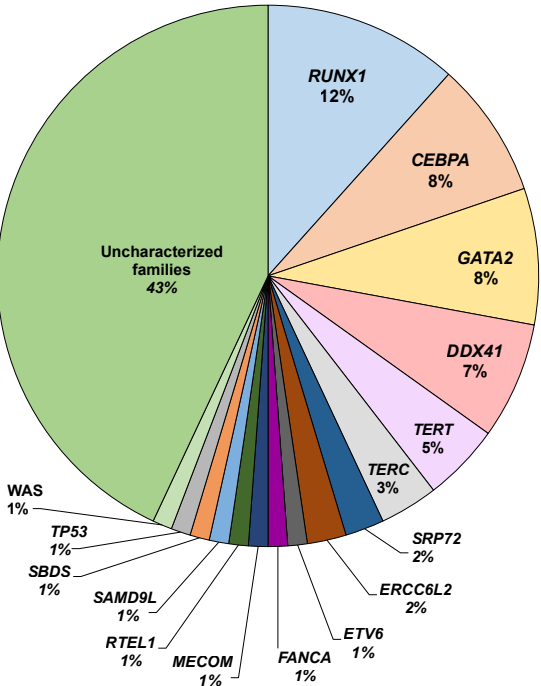
Figure 4: *DHX34* variants fail to phosphorylate UPF1. a, Cartoon depicting the domain structure of *DHX34* indicating the position of the reported variants. b, HEK293T cells depleted of *DHX34* with a specific siRNA or transfected with a scrambled non-targeting siRNA (-) were co-transfected with FLAG-UPF1 and siRNA-resistant wild-type (WT) T7-DHX34 or the indicated *DHX34* variants (including an empty vector plasmid (-) as a control on lanes 1-2). The catalytic inactive *DHX34* mutant K191A served as a negative control (lane 9). Phosphorylated UPF1 was detected with a phospho-(Ser/Thr) ATM/ATR substrate antibody and the

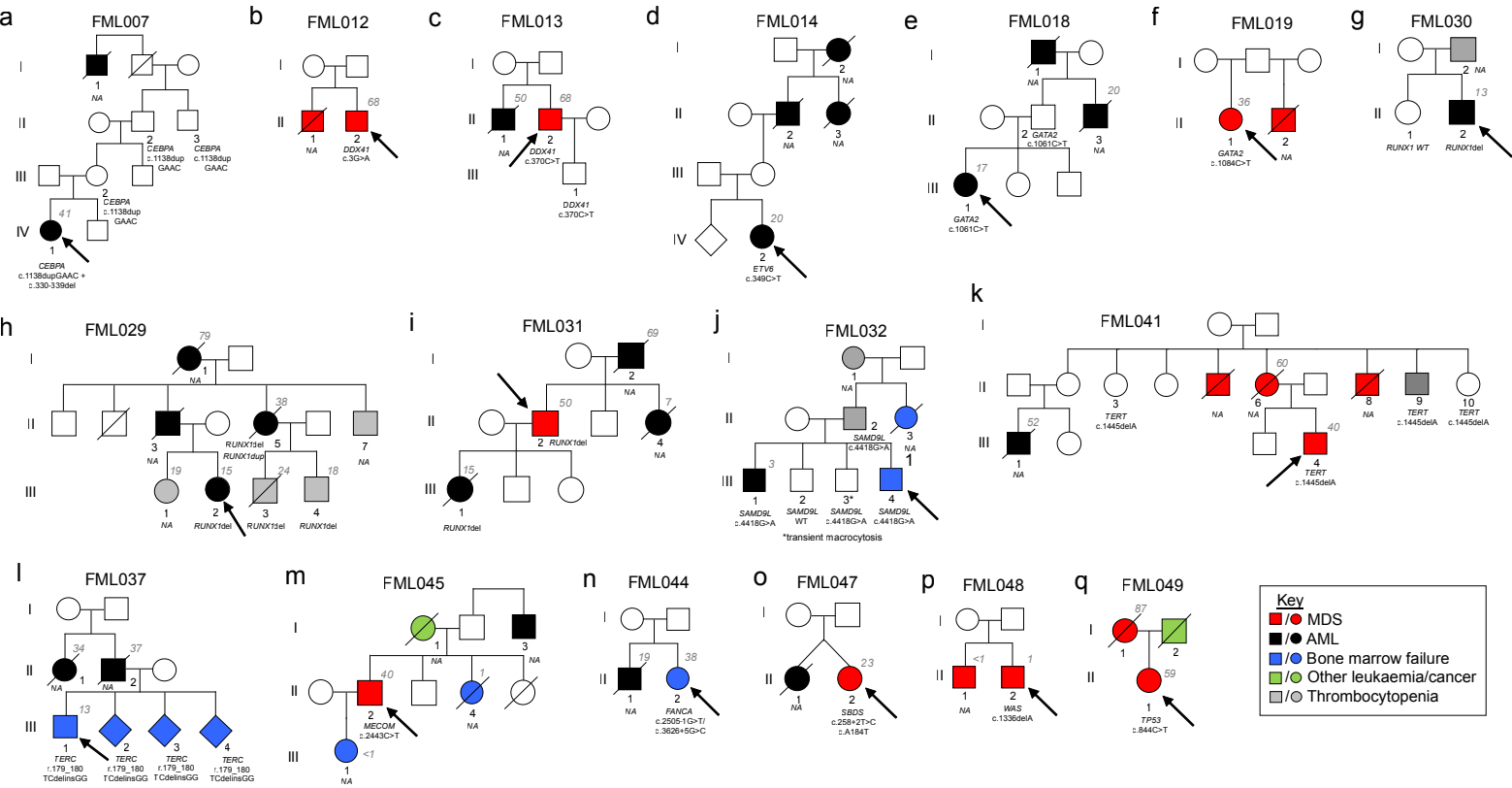
phospho-FLAG-UPF1 signal was normalized to the levels of UPF1 recovered in the IP. Inputs (0.5%) (upper panel) and Anti-FLAG -Immunoprecipitates (20%) (lower panel) were probed for the indicated proteins. c, Quantification of the Western Blot signal, as shown in panel b. Mean values \pm standard deviations from at least two independent experiments are shown. d, Analysis of T7-DHX34 (wild-type protein (WT) and variants) binding to FLAG-UPF1. HEK293T cells were transfected with wild-type T7-DHX34 or *DHX34* variants and FLAG-UPF1. Inputs (0.5%) and Anti-T7 -Immunoprecipitates (20%) were probed for the presence of UPF1. Uncropped Western blots are provided as a Source Data file.

a



b





CLASSICAL INHERITED BMF SYNDROMES

Congenital neutropenia/
Shwachman-Diamond Syndrome

SBDS
SRP72
WAS

Fanconi anaemia

FANCA

Pancytopenia/BMF

ERCC6L2
ETV6
GATA2
MECOM
RUNX1
SAMD9L

Constitutional
thrombocytopenia

DDX41

Dyskeratosis congenita

RTEL1
TERC
TERT

Li-Fraumeni Syndrome

TP53

FAMILIAL MDS/AML

CEBPA

DHX34

DNAH9

NAPRT1

SH2B3

OTHER INHERITED SYNDROMES ASSOCIATED WITH HAEMATOLOGICAL DISEASE

ADA

T(-), B(-), NK(-) severe combined immunodeficiency

GP6

Platelet-type bleeding disorder-11

IL17RA

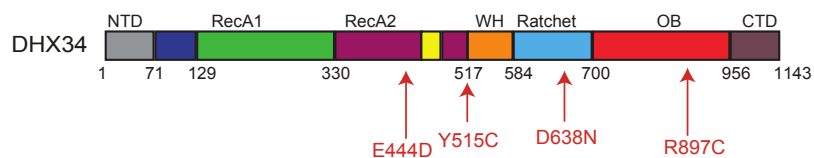
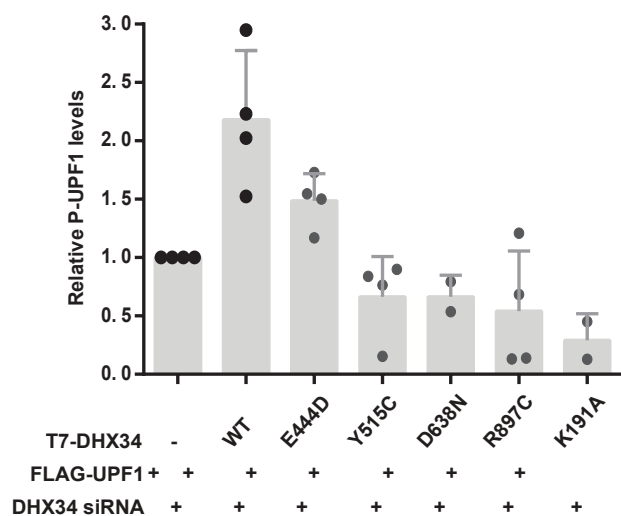
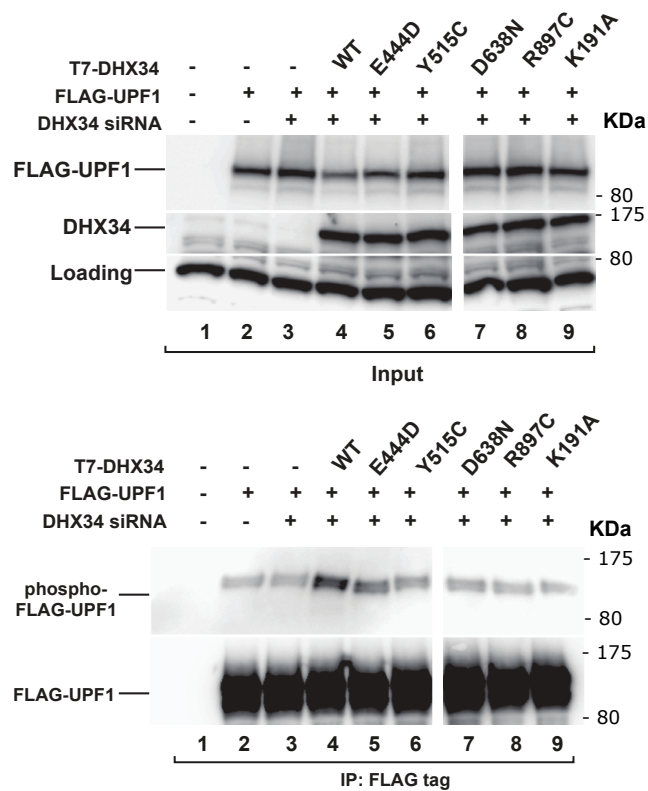
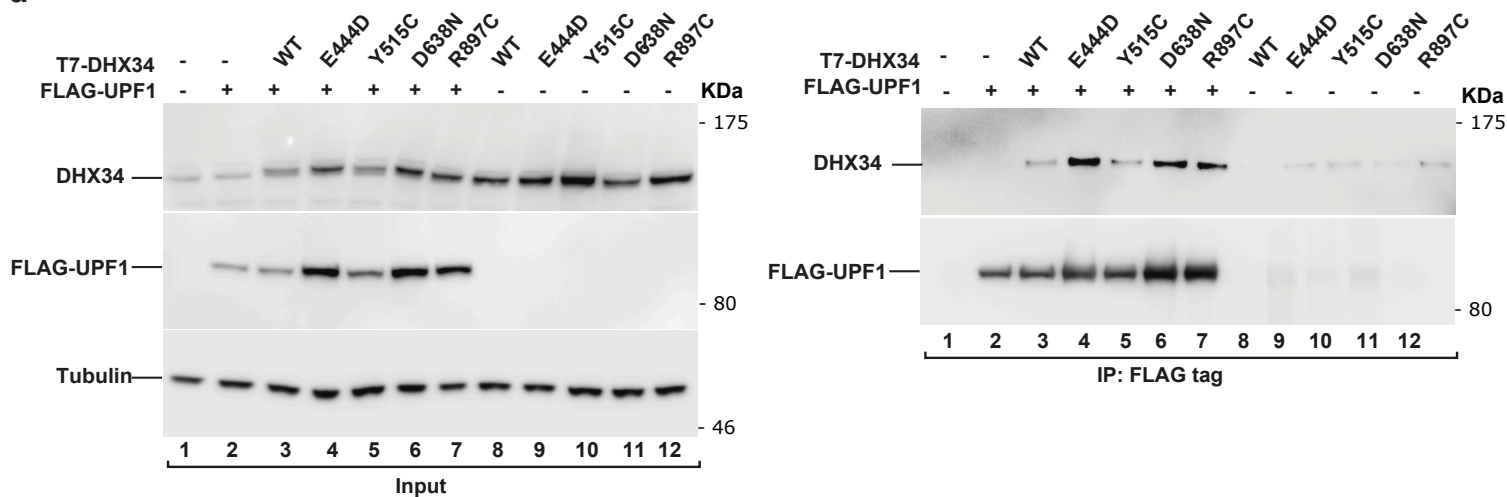
Immunodeficiency-51

PRF1

Familial hemophagocytic lymphohistiocytosis-2

SEC23B

Congenital Dyserythropoietic Anemia Type II

a**c****b****d**

GROUP	DESCRIPTION	GENES		NUMBER OF FAMILIES
GROUP 1	Families with variants in known genes	High level of evidence for gene-disease association.	<i>ANKRD26, CEBPA, DDX41, ETV6, GATA2, RUNX1, TERC, TERT, TP53</i>	39 (45%)
		Moderate level of evidence for gene-disease association.	<i>ACD, CHEK2, RTEL1, SAMD9, SAMD9L, SRP72</i>	4 (5%)
		Genes emerging from basic research or mutated in other inherited hematological syndromes with high risk of MDS/AML.	<i>ATG2B/GSKIP, ERCC6L2, FANC genes, MBD4, MECOM, SBDS, WAS</i>	6 (7%)
GROUP 2	Families where the specific gene variants have not been established	Unknown		37 (43%)

Table 1: Genetic classification of MDS/AML families

Table 2: Summary of FML families

CHARACTERISTICS	NUMBER OF FAMILIES (%)
CLINICAL PHENOTYPE	
MDS	12 (14)
AML	17 (19.8)
MDS/AML	18 (20.9)
MDS/AML/TCP	15 (17.4)
MDS/AML/BMF	24 (27.9)
FAMILY HISTORY OF HEMATOLOGICAL DISEASE	86 (100)
CONSANGUINITY	3 (3.5)
OTHER MALIGNANCIES/DISORDERS	
Non-hematological cancers	12 (14)
Neurological disorders	7 (8.1)
Other hematological malignancies (CML, ALL, Non-Hodgkin's lymphoma)	3 (3.5)
Pulmonary fibrosis	2 (2.3)
Liver disease	2 (2.3)

Table 3: Genes mutated in the 17 unreported Group 1 families

FAMILY	GENE	VARIANT	VAF	TRANSCRIPT ACCESSION NUMBER	ExAC FREQUENCY	ACMG STATUS	ASSOCIATED NON- HEMATOLOGICAL FEATURES
FML007	<i>CEBPA</i>	CEBPA: c.985_988dupGAAC: p.Gln330Argfs*74	NA	ENST00000498907	NO/NO	Pathogenic	NO
FML012	<i>DDX41</i>	DDX41: c.3G>A:p.Met1?	0.454	ENST00000507955	5.11E-05	Likely pathogenic	NO
FML013	<i>DDX41</i>	DDX41: c.370C>T:p.Arg124X	0.61	ENST00000507955	NO	Likely pathogenic	NO
FML014	<i>ETV6</i>	ETV6: c.349C>T:p.Leu117Phe	0.48	ENST00000396373	8.24E-06	VUS	NO
FML018	<i>GATA2</i>	GATA2: c.1061C>T:p.Thr354Met (het)	0.62	ENST00000341105	NO	Pathogenic	NO
FML019	<i>GATA2</i>	GATA2: c.1084C>T:p.Arg362X	0.41	ENST00000341105	NO	Likely pathogenic	congenital deafness, vulva in-situ neoplasia
FML029	<i>RUNX1 del</i>	RUNX1 deletion chr21:36349450-36572837	NA	ENST00000300305	NO	Likely pathogenic	NO
FML030	<i>RUNX1 del</i>	RUNX1 deletion chr21:36400658-36972948	NA	ENST00000300305	NO	Likely pathogenic	NO
FML031	<i>RUNX1 del</i>	RUNX1 deletion chr21:36389492-37056053	NA	ENST00000300305	NO	Likely pathogenic	NO
FML032	<i>SAMD9L</i>	SAMD9L: c.4418G>A:p.Ser1473Asn	0.48	ENST00000318238	NO	VUS	NO
FML037	<i>TERC</i>	TERC: r.179_180TCdelinsGG	NA	ENST00000602385	NO	Likely pathogenic	prematurely gray
FML041	<i>TERT</i>	TERT: c.1445delA:p.His482Profs*27	0.49	ENST00000310581	NO	Pathogenic	skin pigmentation abnormalities
FML044	<i>FANCA</i>	FANCA: c.2505-1G>T	0.45	ENST00000389301	NO	Pathogenic	short stature, leucoplakia
	<i>FANCA</i>	c.3626+5G>C	0.51	ENST00000389301	0.000008961	VUS	
FML045	<i>MECOM</i>	MECOM: c.2443C>T; p.Arg815Trp	NA	ENST00000264674	NO	Likely pathogenic	radioulnar synostosis
FML047	<i>SBDS</i>	SBDS: c.258+2T>C	0.54	ENST00000246868	0.003946	Pathogenic	learning difficulties, short stature, dysmorphic facies
	<i>SBDS</i>	c. 183_184delinsCT; p.Lys62X	0.51	ENST00000246868	0.0004118	Pathogenic	
FML049	<i>TP53</i>	TP53:c.C844T:p.Arg282Trp	0.96	ENST00000376701	NO	Likely pathogenic	NO
FML048	<i>WAS</i>	WAS: c.1336delA; p.Lys446fs	1	ENST00000376701	NO	Likely pathogenic	NO

* Both FML037 and FML041 cases had short telomeres, as determined by monochrome multiplex quantitative PCR. Telomere/single gene ratios were 0.70 and 0.54 respectively, both of which lie below the 10th centile of the normal range.